

Figure 1  
Fatty Acid Biosynthetic Pathway

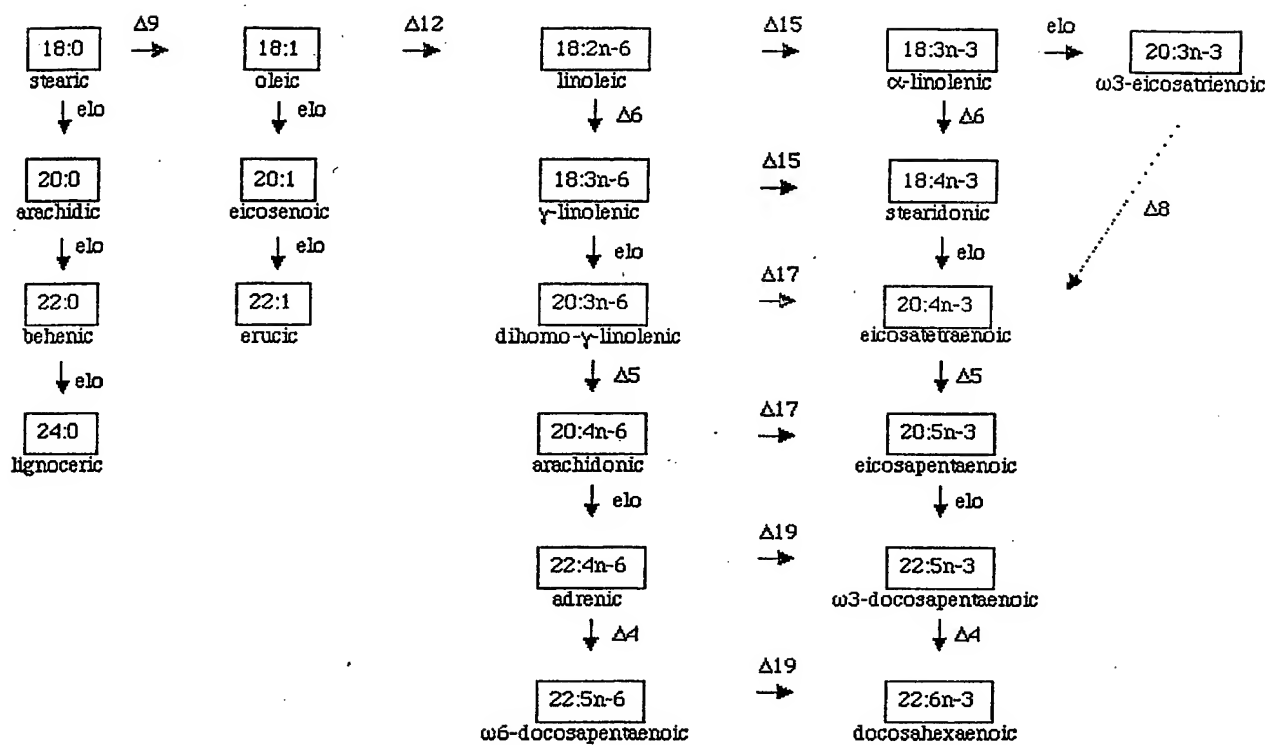


Figure 2

Gene Sequence of Delta 6- Desaturase from *Nycttherus dixlini* (ATCC 56851)

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1  ATGGTCCAGG GGCAAAAGGC CGAGAAGATC TCCTGGGCGA CCATCCGTGA
51  GCACAACCGC CAAGACAACG CGTGGATCGT GATCCACCAC AAGGTGTACG
101 ACATCTCGGC CTTTGAGGAC CAOCCGGGCG SCGTGTCAT GTTCAACGAG
151 GCCGGCGAAG ACBCGACCGA TGCCTTCGCT GTCTTCCACC CGAGCTCGGC
201 GCTCAAGCTC CTCGAGCAGT ACTACGTCGG CGACGTCGAC CAGTCGACGG
251 CGGCGTCGCA CAGTTCGATC TCGGACGAGG TCAAGAAGAG CCACTCGGAC
301 TTCATTGCGT CGTACCGCAA GCTGCGCCTT GAAGTCAAGC GCCTCGGCTT
351 GTAAGACTCG AGCAAGCTCT ACTACCTCTA CAAGTGCAGC TCGACGCTGA
401 GCATTGCGCT TGTGTCGGCG GCCATTGCGC TCCACTTTGA CTCGACGGCC
451 ATGTACATGG TCGCGGCTGT CATCCTTGGC CTCTTTTACC AGCAGTGGGG
501 CTGGCTCGCC CATGACTTTC TGCACCACCA AGTGTGTTAG AACCACTGT
551 TTGGCGACCT CGTCGGCGTC ATGGTCGGCA ACCTCTGGCA GGGCTTCTCG
601 GTGCAATGGT GGAAGAACAA GCACAACACG CACCATGCGA TCCCCAAOCT
651 CCAAGCGACG CCGAGATCG CCTTCCACGG CGACCGGGAC ATTGACAGCA
701 TCGCGATTCT CGGTGGTCG CTCAGATGG CGCAGCACGC GGTGACTCG
751 CCCGTGCGGC TCTTCTTCAT GCGTACCAA GCGTACCTGT ACTTTCCCAT
801 CTTGCTCTTT GCGCGTATCT CGTGGGTGAT CCAGTCGGGC ATGTACGCT
851 TCTACAACGT TGGGCCCAGC GGCACCTTTG ACAAGGTCCA GTACCGGCTG
901 CTCGAGCGCG CCGGCTCCTT CCTCTACTAC GGCTGGAAOC TCGGCTTGT
951 GTACGAGGCC AACATGTCGC TGCTCCAAGC GGCTGCGTTC CTCTTTGTGA
1001 GCCAGGCGTC GTGCGGCGCT TTCTCGCGA TGGTCTTTAG CGTCGGCCAC
1051 AACGGCATGG AGGTCTTTGA CAAGGACAGC AAGCCCCGAT TTTGGAAGCT
1101 GCAAGTGTCT TCGACGCGCA ACGTGACGTC GTGCTCTCTG ATCGACTGGT
1151 TCATGGGCGG CCTCAACTAC CAGATCGACC ACCACTTGTT CCCGATGGTG
1201 CCCCGGCACA ACCTCCCGGC GCTCAACGTG CTCGTCAAGT CGCTCTGCAA
1251 GCAGTACGAC ATCCATACAC ACGAGACGGG CTTCATCGCG GGCATGGGCG
1301 AGGTGCTCGT GCACCTCGAG CGCATCTCGA TCGAGTTCTT CAAGGAGTTT
1351 CCCGCCATGT AA

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### Figure 3

Amino Acid Sequence of Delta 6- Desaturase from *Nyctatherus indicus* (ATCC 56851)

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1  MVQSQKAEKI SWATIREHNR QDNAMIVIMH KYYDISAFED HPGGVVME TQ
51  AGEDATDAFA VFHPSSEAKL LEQYYVGDVD QSTAAVDTSI SDEVKKSQSD
101 FIASYRKLRRL EYKRLGLYDS SKLYYLYKCA STLSTALVSA AICLHEDSTA
151 MYMVAAVILG LEYQCCGMLA KDE DCHQVEE NHLEGDLVGY MYGNIMQSES
201 VQMHKMKHNT HHAIPNIHAT PEIAENGDDP IDTMPILAWS LKMAQHAYDS
251 PVGLEEMRVQ AYLVE PILLF ARISWVIQSA MYAFYNVGPQ GTEDKVQYPL
301 LERAGLLLYY GWNIGLVYAA NMSLLQAAAF LEVSPASCGI FLAMVESVGH
351 NGMEVEIKDS KPDFWKIQVL STRNV TSSLM IDMEFGGLNY QIDMHLEPMV
401 ERHNLPLALNV LVKSLCKQYD IPYHE TGEIA GMAEVVYHLE RISIEEFKEF
451 PAM*

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1054534.01202

Figure 4

Gene Sequence of Delta 5- Desaturase from *Nitrobacter dinitrogen* (ATCC 56851)

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1  ATGGCCCCGC AGACGGAGCT CCGCCAGCGC CACGCCGCCG TCGCCGAGAC
51  GCCGGTGGCC GGCAGGAAAG CCTTTACATG GCAGGAGGTC GCGCAGCACA
101 ACACGGCGGC CTCGGCCTGG ATCATTATCC GCGGCAAGGT CTACGACGTG
151 ACCGAGTGGG CCAACAAGCA CCCCGGCGGC GCGGAGATGG TGCTGCTGCA
201 CGCGGCTCGC GAGGCCACCG ACACGTTCGA CTGTACCAC CCGTTCAGCG
251 ACAAGGCCGA GTCGATCTTG AACAAATATG AGATTGGCAC GTTCACGGGC
301 CCGTCCGAGT TTCCGACCTT CAAGCCGGAC ACGGGCTTCT ACAAGGAGTG
351 CCGCAAGCGC GTTGGCGAGT ACTTCAAGAA GAACAACCTC CATCCGCAGG
401 ACGGCTTCCC GGGCCTCTGG CGCATGATGG TCGTGTGTTG GGTGCGCGGC
451 CTCGCTTGT ACGGCATGCA CTTTTCGACT ATCTTTGCGC TGCAGCTCGC
501 GGGCGCGGCG CTCCTTGGCG TGTGCCAGGC GCTGCCGCTG CTCACGTCAC
551 TGCACGACTC GTCGCAGCGC TCGTACACCA ACATGCCGTT CTTCATTAC
601 GTCGTGGGCC GCTTTGCCAT GGAAGGTTT GCCGGCGGCT CGATGGTGTG
651 ATGGCTCAAC CAGCACGTGC TGGGCCACCA CATCTACAGC AACGTGCGCG
701 GCTCGGACCC GGATCTTCGG GTCAACATGG ACGGCGACAT CCGCCGCATC
751 GTGAACCGCC AGGTGTTCCA GCGCATGTAC GCATTCCAGC ACATCTACCT
801 TCCGCGGCTC TATGGCGTGC TTGGCCTCAA GTTCCGATC CAGGACTTCA
851 CCGACACGTT CGGCTCGCAC ACGAACGGCC CGATCCGCGT CAACCCGCAC
901 GCGCTCTCGA CGTGGATGGC CATGATCAGC TCCAAGTCGT TGTGGGCTT
951 CTACCGCGTG TACCTTCCGC TTGCCGTGCT CCAGATGCCC ATCAAGACGT
1001 ACCTTGGGAT CTTCTTCCTC GCGGAGTTTG TCACGGGCTG GTACCTCGCG
1051 TTCAACTTCC AAGTAAGCCA TGTCTCGACC GAGTGCGGCT ACCCATGCGG
1101 CGACGAGGCC AAGATGGCGC TCCAGGACGA GTGGGCAGTC TCGCAGGTCA
1151 AGACGTGCGT CCACTACGCC CATGGCTCGT GGATGACGAC GTTCCTTGCC
1201 GCGCGCTCA ACTACAGGT CGTGACCCAC TTGTCCCCA GCGTGTGCA
1251 GTACCACTAC CCGGCGATCG CGCCATCAT CGTGCAGCTC TGCAAGGAGT
1301 ACAACATCAA GTACGCCATC TTGCCGGAAT TTACGGCGGC GTTCGTGCGC
1351 CACTTGAAGC ACCTCCGCAA CATGGGCCAG CAGGCGATCG CCGCCAGCAT
1401 CCACATGGGC TAA

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10054534.012202

# Figure 5

Amino Acid Sequence of Delta 5- Desaturase from *Styrrubacter lactum* (ATCC 56851)

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1  MAPQTE LRQR HAAYAETPVA GKKAETWQEV AQHNTAASAM IIRGKYVDY
51  TEWANKHPGG REMVLHAGR EATDTEDSYH EFSDKAESIL NKYEIGTF TG
101 ESEFPTFKED TGFYKECRKR VGEYFKQNNL HPQDGF PGLW RMMVVEAVAG
151 LALYGMHE ST IFALQLAARA LFGVCQALPL LHMMDSSHA SYTWMEF EHY
201 VVGREAMOME AGGSMVSHLN QHYVGHHIYT NVAGSDPDLP VMMDGDIARI
251 VNRQVEQPMY AFQHIYLPPL YGVIGLKERI QDETDTEGSH TNGPIRVNPH
301 ALSTMMAMIS SKSEMAFYRY YLPLAVLQMP IKTYLAIEFL AEFVTGMYLA
351 ENFQVSHVST ECGYPCGDEA KMALQDEWAV SQVKTSVDYA HGSMTTFELA
401 GALEYQVYH HLFPSVQYHY PAIAPITVDV CKEYNKVAI LPDETAAEVA
451 KLEKIDRMMSQ QGIAATHMS *
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Figure 6

Gene Sequence of Delta 5- Desaturase from *Thiomargarita namata* (ATCC 34304)

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1   ATGGGACGCG GCGGCGAAGG TCAGGTGAAC AGCGCGCAGG TGGCACAAGG
51  CGGTSCGGGA ACGGGAAAGA CGATCCTGAT CGAGGGCGAG GTCTACGATG
101 TCACCAACTT TAGGCACCCC GGCGGGTCGA TCATCAAGTT TCTCACGACC
151 GACGSCACCG AGGCTGTGGA CGCGACGAAC GCGTTTCGCG AGTTTCACTG
201 CCGGTCGGGG AAGGCGGAAA AGTACCTCAA GAGCCTGCCC AAGCTCGGCG
251 CGCGAGACAA GATGAAGTTT GAGGCCAAGG AGCAGGCCCG GCGCGACGCG
301 ATCAGCGGAG ACTACGTCAA GCTGCGCGAG GAGATGGTGG CCGAGGGGCT
351 CTTCAAGCCC GCGCCCCCTC ACATTGTCTA CAGGTTTGGG GAGATCGCAG
401 CCCTGTTGCG GGCTCTGTTT TAOTGTTTTT CGATGCGCGG AAACGTGTTT
451 GCGACGCTCG GCGGCATCGC AGTCGGGGGG ATCGCGCAGG GCGGCTGCGG
501 CTGGCTCATG CAAGAGTGGG GACACTTCTC GATGACCGGG TACATCCCGC
551 TTGACGTGCG CCGCAGGAG CTGGTGTACG GCGTGGGGTG CTGATGTGCG
601 GCGAGCTGGT GGCGCTTCA GCACAAACAG CACCACGCGA CCGCGCAGAA
651 ACTCAAGCAC GAGTTCGACC TCGACACCTT GCGGCTCGTT GCGTTCAACG
701 AGAAGATGCG CGCAAGGTG CGCCCGGGCT CGTTCCAGGC CAAGTGGCTC
751 TCGGCGCAGG CGTACATTTT TGCGCCGGTG TGCTGCTTCC TGGTGGTCT
801 CTTCTGGACC CTGTTTCTGC ACOCGCGCCA CATGCCGCGC ACGAGCCACT
851 TTGCTGAGAT GGCGCCGCTC GCGGTGCGCG TGCTGGGCTG GGCGGCGCTC
901 ATGCACTCGT TCGGGTACAG CCGGAGCGAC TGCTTCGGTC TCTACATGGC
951 CACCTTTGGC TTTGGCTGCA CCTACATCTT CACCAACTTT GCGGTCAAGC
1001 ACAGCACCT CAGCTCACC GAGCCGGACG AGTTCTTCCA CTGGGTCGAG
1051 TACGCCGCGC TGCACAGGAC CAACGTGTCC AACGACTCGT GGTTCATCAC
1101 CTGGTGGATG TCGTACCTCA ACTTTCAGAT CGAGCACCAC CTCTTCCGT
1151 CGCTGCCCCA GCTCAACGCC CCGCGCTCG CCGCGCGCT CCGCGCCCTC
1201 TTCGAGAAAG ACGGCATGGC TTACGACGAG CGCCGTAACC TTACGCGCT
1251 TGGGACACG TTTGCCAACC TGACGCGCT GGGCCAAAC GCGGGCCAGG
1301 GGGGCGCAA GCGGCTTAG

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10054534.01202

# Figure 7

Amino Acid Sequence of Delta 5- Desaturase from *Thiostrepton* (ATCC 34304)

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1  MGRSGEGQVN SAQVAPGGAG TRKTILIEGE VYDVTNERHP GGSIIKE LTT
51  DGTEAYDATN AEREHCRSG KAEKYLKSLP KIGAPSKMKE DAKEQARRDA
101 ITRDYVKLRE EMVAEGLEKP APLHIVYREA EIAALEAASE YLF SMRGNVE
151 ATLAALAVGG IAQSRCGHIM HECGHE SMTG YIPLDVRLQE LYYGVGC SMS
201 ASWVRVQDNK HHATPQKLKH DVLDTLEPY AFNEKIAKV RPSSEQAKMI
251 SAQAYIFAPV SCFLVGLEWT LEH ERHMER TSHEAEMAV AVR VVGMAAL
301 MHSFGYSGSD SEGLYMATFG FGCTYIFTNE AVSMTHIDVT E PDEF LHHVE
351 YALHTTNY S NDSMEITWHM SYLNEQIEHH LEPSLEQLNA PRVAPRVRAI
401 FEKHGMAYDE RPYLTALGDT E ANLHVGQN AGQAAAKAA

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Figure 8

1 GAATTCACCA TGGTTCGGG AGCACAGGA GAGCAAGGC AGGCCACAGA  
 51 GCTGAAGAGC AGCCCAAGTG AGCAGCGTAA GGTGTGCTC ATTGACGGGC  
 101 AGGTGTACGA TGCAACCAAC TTCAGGCATC CTGGTGGCTC CATCATCAA  
 151 TATTTGTGCA CCGATGGCAA GGAGGTAGTT GATGCAACCG AAGCGTACAA  
 201 GGAGTTCAC TGCAGATCCT CGAAGGGCGT CAAGTACCTC AACTCCCTGC  
 251 CAAAGATCGA CGGCCCAATC AAGTACAAAT ACGACGCAAA GGAGCAGGCT  
 301 CGCCATGACA AACTCACGAG GGAGTATGTA GCTCTCGCG AACAGCTCGT  
 351 CAAGGAGGGA TACTTTGACC CCAGCCCGCT CCACATTATC TACAGATGCG  
 401 CCGAGTTGGC AGCCATGTTT GCTCTCTCGT TCTACCTTTT CTCCTTCAAG  
 451 GGTAACGTCA TGGCCACTAT TGCTGCCATC GTGATTGGGG GGTGCGTGCA  
 501 GGGTCGTTGT GGGTGGCTCA TGCATGAAGC TGGCCACTAC AGCATGACCG  
 551 GAAACATCCC TGTTGACTTG CGCCTTCAAG AGTTTTGTA CGGAATTGGG  
 601 TGTGGCATGA GCGGGGCTTG GTGGAGAAGC CAGCACAAAC AGCACCACGC  
 651 CACCCCCCAA AAGCTCAAGC ATGACGTTGA TTTGGACACT CTTCTCTTTG  
 701 TCGCCTGGAA CGAGAAATTT GCCCGTCGCG TCAAGCCAGG TAGCTTCCAG  
 751 GCAAAGTGGC TTCACTCTCA CTTTGTACTT GCATCCTCGC CACATGATCC  
 801 TCTCGTTGGT CAACCTCGAG ATATTTTCTG TCGCTCTGCG CTACGTATGC  
 851 GCACCAAGCG CAACCTCGAG CATGGGCTAC ACTGTGCGAG AGTCTCTGGG  
 901 TGGTTCTCGC TTTCTTTTGG GACTTGGCTG TACCTACATC TTTACGCAAT  
 951 TCTCTATGTG CTTACTTTTG GACTTGGCTG TACCTACATC TTTACGCAAT  
 1001 TTGCTGTAAG CCACACCCAC TTGCCAGTGT CCGAGGAGGA CGAGTACCTG  
 1051 CACTGGGTG AGTACGCTGC GCTGCACACC ACGAACGTTG CCATCGACTC  
 1101 GTACGTTGTC ACCTGGCTGA TGAGCTACCT CAACTTTTCAG ATCGAGCACC  
 1151 ACTTGTTCCT TTGCTGCCCG CAGTTCCGCC ACCGTGCAAT CTCCTTCTGGC  
 1201 GTCAAGAAAC TTTTCGAGGA CAATGGTCTG GTATACGACG CCCGCTCATA  
 1251 CGTCCAGGCG CTCAGGATA CCTTCGGCAA CTTACACGAA GTGGGCGTCA  
 1301 AGCTGGCCA AGCTGCCAAG AGCGAGTAAG ATCTCGAG

Start/stop underlined



Figure 9

1 MGRGAQGEPR QATELKSSPS EQRKVLIDG QLYDATNFRH PGSSIICYLC  
 51 TDGKEVV DAT EAYKEFHCRS SKAVKYLNSL PKIDGPIKYK YDAKEQARHD  
 101 KLTREYVALR EQLVKEGYED PSPLHIIYRC AELAAMEFALS FYLFSEKGNV  
 151 MATIAAIVIG GCVQGRCGWL MHEAGHYSMT GNIPVDLRQ EFLYGIGCGM  
 201 SGAWWRSQHN KHHATPQKIK HDVDLDTLPL VAWNEKIARR VKPGSFQAKW  
 251 LHLQGYIFAP VSCLLVGLFW TLYLHPRHMI RTKRNFEIFS VALRYVCWFS  
 301 LLLSMGYTVG ESLGLYVLTFF GLGCTYIIFTH FAVSHTHLPV SEEDEYLHWV  
 351 EYRALHTTNV AIDSYYVTWL MSYLNFOIEH HLFPCCPQFR HPAISSRVKK  
 401 LFEDNGLVYD ARSYVQALKD TFGNLHEVGV NAGQAAKSE

Figure 10

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1  CCATGGGCGG CGGGCGCGAG AAAAGCGAGG TGGACCAGGT GCAGCCACAA
51  AAGACCGAGC AGCTCCAGAA GGCCAAAGTGG GAGGATGTTG TTCGCATCAA
101  TGGAGTCGAA TACGACGTCA CGGACTATCT CAGAAAAACAC CCTGGTGGCA
151  GCGTGATCAA GTACGGGCTT GCCAACACCG GCGTGATGC CACGTCCCTC
201  TTTGAAGCGT TCCACATGCG CTCAAAGAAG GCTCAGATGG TGCTCAAGTC
251  TCTCCCAAAG CGTGCTCCGG TCCTCGAGAT CCAGCCAAAC CAGCTTCCAG
301  AGGAGCAGAC CAAGGAGCGG GAGATGCTGC GTGATTTTAA AAAATTTGAG
351  GATGAGATTC GCCGGGATGG ATTGATGGAA CCTTCCTTCT GGCAFCGCGC
401  TTACAGATTG TCAGAGCTTG TAGGTATGTT CACGCTCGGC CTCTACCTCT
451  TCTCGTTAAA CACTCCTCTG TCTATTGCTG CTGGTGTCTT CGTCCACGGT
501  CTCTTTGGTG CATTCCTGCG ATGGTGCCAG CATGAGGCAG GCCACGGCTC
551  CTTTTTTTAC AGCCTTTGGT GGGGCAAGCG TGTACAGGCC ATGTTGATCG
601  GGTTCGGTCT AGGAACATCC GCGACATGT GGAACATGAT GCACAACAAG
651  CATCATGCTG CCACCCAAA GGTTCATCAC GACCTTGACA TTGACACAAC
701  TCCTTTTGTA GCTTTCCTCA ACCTGCAAT TGAGAAAAAC AGATGGAAGG
751  GCTTTTCCAA GGCCTGGGTC CGCTTTCAGG CTTTACGTT CATTCCTGTC
801  ACCAGCGGCA TGATCGTCAT GCTGTTCTGG CTGTTTTTTC TCCACCCCTG
851  CCGCGTCGTT CAAAAGAAGA ACTTTGAGGA GGGTTTTTGG ATGCTGTGGA
901  GCCACATTGT GCGCACCTAT CTCCTCCACC TTGTGACCCG CTGGGAGAGC
951  CTCGCTGCAT GCTACCTTGT TTTGGCCACT TTTGCTCTC CCACACTCAT ATGGACATTG
1001  TATGTAATTG TTTGGCCACT TTTGGCCACT TTTGCTCTC CCACACTCAT ATGGACATTG
1051  TGGAGCGCGA CGTGCAATAG AACTGGGTCA GGTACGCTGT TGACCCACCT
1101  GTTGACATCA GCCCATCCAA CCGCTCGTG TGCTGGGTCA TGGGTTACCT
1151  CAACATGCAG ACCATCCACC ACTTGTGGCC TGCCATGCCC CAGTACCACC
1201  AGGTCGAGGT CTCACGCCGC TTGCCCCTCT TCGCCAAAAA ACACGGCCTC
1251  AACTACCGCG TCGTCTCTTA CTTTGAGGCT TGGCGCCTGA TGCTCCAAAA
1301  TCTTGCTGAC GTCGGTTCCC ACTACCATGA GAACGGTGTG AAGCGCGCCC
1351  CAAAGAAAGC CAAGGCGCAG TAGAAAGCTA T

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Start/stop underlined

Figure 11

1 MGRGKSEV DQVQPKTEQ LQAKWEDVV RINGVEYDVT DYLRKHFGGS  
51 VIKYGLANTG ADATSLFEAF HMRSKKAQMV LKSLPKRAPV LEIQPNQLPE  
101 EQTKEAEMLR DFKKFEDEIR RDGLMEPSFW HRAYRLSELV GMFTLGLYLF  
151 SLNTPLSIAA GVLVHGLFGA FCGWCQHEAG HGSFFYSLWW GKRVOAMLIG  
201 EGLGTSGDMW NMMHNKHAA TQKVHHDLDI DTPPFVAFEN TAFEKNRWKG  
251 FSKAWVRFOA FTFIPVTSGM IVMLFWLFFL HPRRVQKKN FEEGFWMMLSS  
301 HIVRTYLFHL VTGWESLAAC YLVGYWACMW VSGMYLFGHF SLSHTHMDIV  
351 EADVHKNVR YAVDHTVDIS PSNPLVCWM GYLNMQTIHH LWPAMPQYHQ  
401 VEVSRRFAIF AKKHGLNYRV VSYFEAWRLM LQNLADVGSH YHENGVKRAP  
451 KKAKAQ

Figure 12

pRAT-2a	1	MGRGAQGEPRQATELKSSPSEQRKVLLIDGQLYDATNFRHPGGSI	45
pRAT-2c	1	MGRGAQGEPRQATELKSSPSEQRKVLLIDGQLYDATNFRHPGGSI	45
pRAT-2a	46	IKYLC TDGKEVVDAT EAYKEFHCRSSKADKY LNSLPKIDGPIKYK	90
pRAT-2c	46	IKYLC TDGKEVVDAT EAYKEFHCRSSKADKY LNSLPKIDGPIKYK	90
pRAT-2a	91	YDAKEQARHDKLTREYVALREQLVKEGYFDPSPLHIIYRCAELAA	135
pRAT-2c	91	YDAKEQARHDKLTREYVALREQLVKEGYFDPSPLHIIYRCAELAA	135
pRAT-2a	136	MFALSFYLF SFKGNVVA TIAAIVIGGC VQGRCGWL MHEAGHY SMT	180
pRAT-2c	136	MFALSFYLF SFKGNVVA TIAAIVIGGC VQGRCGWL MHEAGHY SMT	180
pRAT-2a	181	GNIPVDLR LQEEFLYGIGCGMSGAWRRRQH NKHHA TPQK LKHHDVDL	225
pRAT-2c	181	GNIPVDLR LQEEFLYGIGCGMSGAWRRRQH NKHHA TPQK LKHHDVDL	225
pRAT-2a	226	DTLPLVAWNEK IARRVKPGS FQAKWPHLQGY I FAPVSC L L VGLFW	270
pRAT-2c	226	DTLPLVAWNEK IARRVKPGS FQAKWPHLQGY I FAPVSC L L VGLFW	270
pRAT-2a	271	TLYLHPRRHM IRTKRNFE IFSVALRYVCWFSL L L S MG YTVGES LGL	315
pRAT-2c	271	TLYLHPRRHM IRTKRNFE IFSVALRYVCWFSL L L S MG YTVGES LGL	315
pRAT-2a	316	YVLTFFGLGCTY IFTTHFAVSH THLPVSEEEDEY LHWVEY AALHTTNV	360
pRAT-2c	316	YVLTFFGLGCTY IFTTHFAVSH THLPVSEEEDEY LHWVEY AALHTTNV	360
pRAT-2a	361	AIDSYYVVTWLM SYLNFQIEHHLFPCCPQFRHPA I SSRVKKLFEDN	405
pRAT-2c	361	AIDSYYVVTWLM SYLNFQIEHHLFPCCPQFRHPA I SSRVKKLFEDN	405
pRAT-2a	406	GLVYDARS YVQALKDTFGNLHEVGVNAGQAAKSE	439
pRAT-2c	406	GLVYDARS YVQALKDTFGNLHEVGVNAGQAAKSE	439

Figure 13

pRAT-1a	1	MGRGGEKSEVDQVQPQKTEQLQKAKWEDVVRINGVEYDVTDYLR	44
pRAT-1b	1	MGRGGEKSEVDQVQPQKTEQLQKAKWEDVVRINGVEYDVTDYLR	44
pRAT-1a	45	KHPGGSVIKYGLANTGADATSLFEAFHMRSKKAQMVLKSLPKRA	88
pRAT-1b	45	KHPGGSVIKYGLANTGADATSLFEAFHMRSKKAQMVLKSLPKRA	88
pRAT-1a	89	PVLEIQPNQLPEEQTKAEMLRDFKFFEDEIRRDGLMEPSFWHR	132
pRAT-1b	89	PVLEIQPNQLPEEQTKAEMLRDFKFFEDEIRRDGLMEPSFWHR	132
pRAT-1a	133	AYRLSELVGMFTLGLYLFSLNTPLSLAAGVLVHGLFGAFCGWCC	176
pRAT-1b	133	AYRLSELVGMFTLGLYLFSLNTPLSLAAGVLVHGLFGAFCGWCC	176
pRAT-1a	177	HEAGHGSFFYSLWWGKRQAMLIGFGLGTSGDMWNMMHNKHHAA	220
pRAT-1b	177	HEAGHGSFFYSLWWGKRQAMLIGFGLGTSGDMWNMMHNKHHAA	220
pRAT-1a	221	TQKVHHDDLIDITTPFFVAFNATAFEKNRWKGFSAWVRFQAFIFI	264
pRAT-1b	221	TQKVHHDDLIDITTPFFVAFNATAFEKNRWKGFSAWVRFQAFIFI	264
pRAT-1a	265	PVTSGMIVMLFWLFFLHPRRVVQKKNFEEGFWMSSSHIVRTYLF	308
pRAT-1b	265	PVTSGMIVMLFWLFFLHPRRVVQKKNFEEGFWMSSSHIVRTYLF	308
pRAT-1a	309	HLVTGWESLAACYLVGYWACMWVSGMYLFGHFSLSHTHMDIVEA	352
pRAT-1b	309	HLVTGWESLAACYLVGYWACMWVSGMYLFGHFSLSHTHMDIVEA	352
pRAT-1a	353	DVHKNNWVRYAVDHTVDISPSNPLVCWVMGYLNMQTIHHLWPAMP	396
pRAT-1b	353	DVHKNNWVRYAVDHTVDISPSNPLVCWVMGYLNMQTIHHLWPAMP	396
pRAT-1a	397	QYHQVEVSRRF A IFAKKHGLN YRVVSYFEAWRMLQN LADVGS H	440
pRAT-1b	397	QYHQVEVSRRF A IFAKKHGLN YRVVSYFEAWRMLQN LADVGS H	440
pRAT-1a	441	YHENGVKRAPKKAKAQ	456
pRAT-1b	441	YHENGVKRAPKKAKAQ	456

Figure 14

1 ATGGTGGCAG GCAAATCAGG CGCTGCGGCG CACGTGACTC ACAGCTCGAC  
51 ATTGCCCCGT GAGTACCATG GCGCGACCAA CGACTCGCGC TCTGAGGCGG  
101 CCGACGTACG CGTCTCTAGC ATCGATGCTG AAAAGGAGAT GATCATCAAC  
151 GGCCGCGTGT ATGACGTGTC GTCATTTGTG AAGCGGCACC CAGGTGGCTC  
201 GGTGATCAAG TTCCAGCTGG GCGCCGACGC GAGCGACGCG TACAACAACT  
251 TTCACGTCCG CTCCAAGAAG GCGGACAAGA TGCTGTATTG GCTCCCGTCC  
301 CGGCCGCGCG AGGCCGGCTA CGCCAGGAC GACATCTCCC GCGACTTTGA  
351 GAAGCTGCGC CTCGAGCTGA AGGAGGAGGG CTACTTCGAG CCAACCTGG  
401 TGCACGTGAG CTACAGGTGT GTGGAGGTTT TTGCCATGTA CTGGGCTGGC  
451 GTCCAGCTCA TCTGGTCCGG GTACTGGTTC CTCGGCGCGA TCGTGGCCGG  
501 CATTGCGCAG GGCCGCTGCG GCTGGCTCCA GCATGAGGGT GGGCACTACT  
551 CGCTCACCGG CAACATCAAG ATCGACCGG ATCTGCAGAT GGCCATCTAT  
601 GGGCTTGGCT GCGGCATGTC GGGCTGCTAC TGGCGCAACC AGCACAACAA  
651 GCACCACGCC ACGCCGCGA AGCTCGGGAC CGACCCCGAC CTGCAGACGA  
701 TGCCGCTGGT GGCCTTCCAC AAGATCGTCG GCGCCAAGGC GCGAGGCAAG  
751 GGCAAGGCGT GGCTGGCGTG GCAGGCGCCG CTCTTCTTTG GCGGGATCAT  
801 CTGCTCGCTC GTCTCTTTG GCTGGCAGTT CGTGCTCCAC CCAACACG  
851 CGCTGCGCGT GCACAATCAC CTGGAGCTCG CGTACATGGG CCTGCGGTAC  
901 GTGCTGTGGC ACCTGGCCTT TGGCCACCTC GGGCTGCTGA GCTCGCTCCG  
951 CCTGTACGCC TTTTACGTGG CCGTGGGCGG CACCTACATC TTCACCAACT  
1001 TCGCCGTCTC GCACACCCAC AAGGACGTCG TCCCGCCAC CAAGCACATC  
1051 TCGTGGGCAC TCTACTCGGC CAACCACACG ACCAACTGCT CCGACTCGCC  
1101 CTTTGTCAAC TGGTGGATGG CCTACCTCAA CTTCCAGATC GAGCACCACC  
1151 TCTTCCCGTC GATGCCGCGA TACAACCACC CCAAGATCGC CCCGCGGGTG  
1201 CGCGCGCTCT TCGAGAAGCA CGGGGTCGAG TATGACGTCC GGCCATACCT  
1251 GGAGTGTTTT CGGGTCACGT ACGTCAACCT GCTCGCCGTA GGCAACCCGG  
1301 AGCACTCCTA CCACGAGCAC ACGCACTAG

202270-4E54500F

Figure 15

1 MVAGKSGAAA HVTHSSTLPR EYHGATNDSR SEAADVTVSS IDAEKEMIIN  
51 GRVYDVSSFV KRHPGGSVIK FQLGADASDA YNNFHVRSKK ADKMLYSLPS  
101 RPAEAGYAQD DISRDFEKLRL LELKEEGYFE PNLVHVSYRC VEVLAMYWAG  
151 VQLIWSGYWF LGAIVAGIAQ GRCGWLQHEG GHYSLTGNIK IDRHLQMAIY  
201 GLGCGMSGCY WRNQHNKHA TPQKLGTDPD LQTMPLVAFH KIVGAKARGK  
251 GKAWLAWQAP LFFGGIICSL VSFGWQFVLH PNHALRVHNNH LELAYMGLRY  
301 VLWHLAFGHL GLLSSLRLYA FYVAVGGTYI FTNFAVSHTH KDVVPPTKHI  
351 SWALYSANHT TNCSDSPFVN WWMAYLNFQI EHHLFPSMPQ YNHPKIAPRV  
401 RALFEKHGVE YDVRPYLECF RVTYVNLLAV GNPEHSYHEH TH

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